

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGCTCTCCCG
CAGCGCTACCCGCCATGCGCTGCGCTGCCGCCGGCGCTGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAACGCCGACGCCCTGCCACCAGGTGCCGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACGCCGAGATTGCCCTGCTGGAGATC
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGCTGCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGCGACGGGTCTGCCGGTGCACATGGGTACCAAGGGCCGCTGTGCAGCTGACTGATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCAGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACAGTGTGCAGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCAGGGAGCA
CGGACAGTGTGCAGATGTGGACAGTGTGCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCGTGTGTCCTGACGGCTCGAACAGAAACG
GAAGATGCCGTGTGCCGCCAGAGCTGAAGCCACAGAAGGAGAAAGCCCACACAGCT
GCCCTCCCGCAAGACCTGTAATGTGCCGACTTACCCTTAAATTATTCAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCTGCAGTGGACAGCGGGAGAGGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTGTATATTGATACTGTTCTTGTAAATAAAATTGACCATTGTAGGTAAATCAGG
AGGAAAAAAAGGGGGGGCGACTCTAGAGTCGACCTGCAGAAC
TTGGCCGCCATGGCCAACCTGTTATTGCACTTACTGCATTCTAGTTGTGGTTGTCCAAACTC
TCACAAATTTCACAAATAAGCATTTCAGTCACTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATTGCCGCAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGGAAAGAACCCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

SCANNED # 12

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPAPPEAKKPTPCRCRGLVDKFNQGMVDTAKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKCCSPGTYPDCLACQGGSQRPCSG
NGHCSGDGRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCGTLNRDCGECEVGWLDE
GACVDVDECAAEPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACTCGACCTCGTTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCCTCGGCCAGGCCGGAGGCAGCGCCAGCCGTCAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGATGGCCGGAGGAGCGCCTTC
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGAAAGACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCTCACAAAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAACT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGGGTGCCAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTGTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACGCTCAACCACCTGCTTAAATGGAGGGACC
TGTCTACCCCTGGAAAATGTATTGCCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCCTGTCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGGTGCACAT
GGAACCTGCCATGAACCCAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCGAGGAGCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAAATTATTAGCT
TCATTATAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCACTGCTTGGACAGATTATATTATGTCATTGAA
TCAGGTTAAAATTTCACTGAGCTGTTGGCAGATATTTCAAAATTACAATGCAATTGTT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGCAAAATCGTAAGTCACAAGAAT
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GTTTGTACATTAAAAATTGCTCTTAATTAAACTCTCAATACAATATAATTGACCTT
TTACCAATTCCAGAGATTCACTGATTAAAAAAATTACACTGTGGTAGTGGCATTT
AAACAATATAATATTCTAAACACAATGAAATAGGAAATATAATGATGAACTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTTACCTAATAAACATTGAT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTGGC
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

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><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTIQLQTQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIKGSKCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGGTGCGAGGCCAGGGAGGCAGGCCGGCTGG
CCCCAGCCCACACCTCACCAGGGCCCAGGAGCCACC**ATGT**GGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCAGCAGTGTGCCCTGCCCTACCTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCAGGTCTCGACTGCTGCCCTGACTTCTGGACTTC
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTGGAACGTACTGGGACAACGTAAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCTGG**ATG**GGGCATTGCTACCGCCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCCTGTGAGAAGTGGCCAACCTGATTGATGAGCCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCTGCCCCAGAACCTGCTGTCTGTGAC
ACCCACCAGCAGCAGGCTGCCCGGTCTCGATGGTGCCTGGTGGTCTCGT
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACATGACATCTACCAAGGTACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
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CTTGGGAGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAGTCAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCCAACCTCTGGGCC
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGGCCGTCAATGAGTGCAGACATCGAG
AGCTTGTGCTGGCGTCTGGGCCGCTGGCATGGAGGACATGGGTATCACTGAGGCTG
CGGGCACCACGCCGGCTCCGGCTGGATCCAGGCTAACGGCCGGCGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGCGCAGGCCGGCGCCAGGGCGCTAAT
CCCGCGCGGGTTCGCTGACGCAGGCCCGCCTGGGAGGCCGGCAGGGAGACTGGCG
GAGCCCCAGACCTCCCAGTGGGACGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCTCAAGACTACAAAGCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGCTTGCTCCG
TTGCCCAAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTGCACCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC
TAATTGGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT
CCTGGCTCAAGCGGTCCACCTGCCTCCGCCCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAAACAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYCQEQLLCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGCCTTNGCCCCAGAACCTGCTGTCTTGACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACGCCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCTCTGACCCTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCACTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGCACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTCCCCAGGAAGCCTT
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCGACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPafSTLNpVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGACAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGAAGAGCAAAGACTG
CGTGGTCACGGAGATCGTGGAGAACAACTATACTGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGCCCTCACGCCAGGGGCCCGCCAGGCTCCCGCAGCCGAGAAC
CAGCGCGAGGCCACTTCATCAAGGCCCTACCAAGGCCAGCTGCCCTCCCCAACCACGC
CGAGAACAGCAGTCGAGTTGTGGCTCCGCCCGACCAAGCGCACAC
GGCGGCCAGGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGCAGGCCAGATCCCC
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGAAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTGCCGGCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTAGCGACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCAACTCCTCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCCCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCATCCAGT
CATTGGATTGCTGTTATTTTTCTTTTCTTTCCCACCACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTGGCTTATCATTTCCCTGGGGCTACTCACAGGTGTCAAACCTCGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCACCTCACACAACAAACCAATTAAATAATGC
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AATATTGACACCATTTCACGGCTGCTTGCCTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTTCCGGAGGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAACCTGAGCAGTGTGCCTGTTGGGCTTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCTATCGACATGGCCTTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGAGCAGGGAACCTCCTGACCAACAAGGGTATGCCG
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CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGAGGACAACCAGAT
AAACACATTCTTGTACAGCCTCTCAAATCTGCGTAAGCTGAAACGGCTGGATATATCCA
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ACTGCTCGGAATAACCCCTGGTTTGTGACTGCAGTATTAAATGGGTACAGAACGGCTCAA
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG
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CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAAGCTACACGCCTCCAACCTACCCACATCGAAACTCCACGATT
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CAAACTCACATGGGTGAAAATGGGCCACAGTTAGTAGGGGCATCGTTAGGAGCGCATAG
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CACAGACTGCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
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CACACTCGTGTGTGACATAAAGACACCGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCAATTGAAACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG
CTATCTTTCTATTCAAGTTAACACAGTTGTAACCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWP SHGAFFLKS WLIIISL GLY SQV SKLLACPS VCR CDR NFV YCN ERS LT SVPL GIP
EGTV VLYLHNN QINNAGF PAEL HNV QSV HTV YLYGN QLDEF PMNL PKN VRVL HLQ ENNI QT I
SRA ALA QLL KLEEL HLDD NSI STVG VED GA FREA ISL KLL FLS KNHL SSVP VGL PVD LQ ELR
VDEN RIAVI SDMAF QNL TS LERL IVD GNLL TNKG IAEGT FSHT KLKE FSIV RN SL SH PPPD
LPG THLIR LYLQDN QIN HIPL TA FS NL RKL ER LD I SNN QL RML T QGV FDNL SNL QLT AR NN
PWF CD CSIK WVT EWL KYI PSSL NVRG FMC QG PEQ VRGM AVREL NMN LLSCPT TTP GLPL FTP
APST ASPTT QPPT LSIP NPSR SYTP PT PTT SKL PT IP DW DGR ER VT PP I SERI QLS IH FV ND
TSIQ VSWL S LFTV MAYK LTWV KM GHSL VGG I VQER IVS GEK QHLS LVN LE PRST YR I CLV PL
DAF NYRA VE DTIC SEAT THAS YLN NG SNT ASSHE QTT SHSM GSP FLL AGLIGG AVIF VL VVL
LSV FCWHM KK GRY T S QWK YNR GRR KDDY CEAGT KK DNSI LEM TET SFQ I VSL NN DQ LL KG
DFRL QPI YTP NGG INY TDCHI PNN MRY CNSS VP DLE HCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGGGGGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCCACGAGCG
ATCCCCGAGGAAGCCGCGGCCCTCGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC
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GCTTTCTGCTGATCCTCGGACAGATCGCCTCCTCCCTGCCAGGGCAGGGAGGGTCAAGTGGGGAGGTCCATCT
CTAGGGCAGACACGCTCGGACCCACCCGACAGGCCCTCTGGAGAGTTCCTGTGAGAAACAAGGGGGAGACC
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GCACCATGACTGGGCTGGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTCTAAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCGAGGTGGCTGCTA
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GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCACAGCAGTTCAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCCTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGAGGACTACTGTGCCCTAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCTAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGCACAAGGAACAACTACTGTGCACTGAAACAAACCGGGCTGTGAGCATGAGTGCCTAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAAGCCAGTGGACACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAAACACGGAGGATTCCCTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTTGAGTACTGCTGCTGAGTCACATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCCTGTCAGTGCCTGAGGGACACGGCTCCGAGCGATGGGAAGACAGTGTG
CAAAATTGGACTCTTGTGCTCTGGGGGACACGGTTGTGAACATTGCTGTGTAAGCAGTGAAGATTGTTGTG
GCCAGTGTGTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAAGAAGGAAAGATGTCGCAAGCTATAG
ACCATGGCTGTGAAACACATTGTGAAACAGTGAACACTCATACACGTGCGAGTGTGTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAAGGAAGGATGTGCAAAATCAACCCACCATGCTGCAACACATTGTGTTA
ATAATGGGAACTCCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAGAAAT
GCACTGAAGGCCAATTGACCTGGTCTTGATCGATGGATCCAAGAGTCTTGAGAAGAGAATTGAGGTG
TGAAGCAGTTGTCACTGAAATTATAGATTCCCTGACAATTCCCCAAAGCCGCTGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGGCAAAAGACATGAAAAAGCCGTGGCC
ACATGAAATACATGGGAAAGGGCTATGACTGGGCTGGCCCTGAAAACACATGTTGAGAGAAGTAACTCCAAG
GAGAAGGGCCAGGCCCTTCCACAAGGTGCCAGAGCAGCCATTGTTGACCGACGGACGGGCTCAGGATG
ACGTCCTCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGATGCTGTTGGGTTAGGAAAAGCCATTG
AGGAGGAACCTACAAGAGATGCTCTGAGGCCACAAACAGCATTCTTCTATGCCGAAGACTCAGCACAATGG
ATGAGATAAGTGAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACCTGCCAAAACGGTCCAAGGCCAACAGAACTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTGCACTGCAACACAGATATCTGTTGAAGAAGACAATTGTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTCAGGAAGGCCCTTGGAAAGAAAACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCACAGGAAGAAGTAAGAAAATTAAACACAGGCCCTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATCGCTGAGATAAGATGAAGATTAGAAAATCGGCACACATTGTTAGTCATTGATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCCCACAGAACAAAGACAAGAAGTATAACACTAATTGTTAAATTTATCTAGGAAAAAAATCCT
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTGAATATACTGTGGACAC
AACTTGCTTCTGCCCATCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGTTAGAACACTGCCATAGGAAATGCTGTTTTTGTACTGGACTTACCTGATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTATAACATATTAAAATCACCACCTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVFIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAVKMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHFCINIPIGSYVCRKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGCE EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCE HSCVSSEDSFVCQCFCGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLEDGKRCRRKDVKSTHHGCEHICVNNNGNSYICKCSEGTVLAEDGRRCKCTEGPIDLVFVID GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEELQEIASEPTNKHLYAEDFSTMDEISEKLKGICEALEDSDGRQDS PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEEDNLLRSTQKLSHSTKPGSPL EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCA~~GCGGCTGGCTCCGCACGCTCCGGCGTCGCAGCCTCG~~
GCACCTGCAGGTCCGTGC~~GTCCCAGGCTGGCGCCCTGACTCCGTCGGCCAGGGAGGGC~~
CATGATTCCTCCGGGCCCTGGTGACCAACTTGCTGCGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCG~~GGGCCAGCTGCAACTGCACTTGCCCACCGGTTGCAG~~
GCGGTGGAGGGAGGGAA~~GTGGTGCCTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC~~
ATCCCAGCCATGGGAGGTGCC~~CTTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC~~
AGGTGTTGT~~CCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC~~
ATGCCCTCCGGAAC~~CTGTCCCTGCGGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA~~
CAGCTGCTCCGTGA~~ATGTGCAAGACAACAAGCAAATCTAGGGCACAGCATAAAACCT~~
TAGAACTCA~~ATGTACTGGTCCTCCAGCTCCTCATCCTGCCGTCCAGGGTGTGCCCAT~~
GTGGGGCAA~~ACGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCCAATACCA~~
GTGGGATCGGCAG~~CTTCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG~~
GGTCTTAAGC~~CTACCAACCTTCGTCTCATGGCTGGAGTCTATGTCAGGCCAC~~
AATGAGGTGGGACTGCCA~~ATGTAATGTGACGCTGGAGTGCACAGGCCCTGGAGCTGC~~
AGTGGT~~GCTGGAGCTGTTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC~~
TCTTGTACCACGCC~~GGGCAAGGCCCTGGAGGCCAGCAATGATACTAAGGAGGATGCC~~
ATTGCT~~CCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAACATGGGACCC~~
TTCCTCTGT~~CACCTCCGCACGCCCTCCGCCACCCATGGCCCTCCAGGCCTGGTGCAT~~
TGACCCCCACGCC~~CAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT~~
GGGGCCCAC~~CCCTCAACCAATATCCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG~~
CATGGGT~~GCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTATGATGAC~~
CCCACCACT~~CATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTACACTCTAGCAC~~
AGAGGCC~~TGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCAACCTCTC~~
TTTACTGTGGAAAACC~~ATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAAGAGGA~~
AGTGGATCT~~GGATTGGAGGAGCCTCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG~~
CTGAAATTAG~~CTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCTCCAGGC~~
CCCCT~~TGATCTGTACCCACCCATCTAACACCCACCCCTGGCTCCACTCCAGCTCCCTGT~~
ATTGATATAAC~~CTGTCAAGCTGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAATCTC~~
TTATTAAA~~ACTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA~~
TGT~~TTGTATGAAAAA~~

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQS PRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKSSDTISKNGTL
SSVTSARALRPPHGPPRGALTPTPSLSSQALPS PRLPTTDGAHPQPISPIPGVSSGLSR
MGAVPVMVPAQS QAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCA**A**TGAAACGCCTCCGCTCTAGTGGTTTTCCACTTTG
TTGAATTGTTCTATACTCAAAATTGCAAGCACCTGTCTCCAAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGATTTCAGGAAATGGTGTACCAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTG
ACTAACACAGAAGGAAGTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAACTTTAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATATTAGCTGAATCATCTCATTACTAGGTTACAAGAACAA
CTATCTCAGCCAAGGCACCCCTTCTAACACTCAACTCTTACTGAATTGTAACCGTGAAT
AATTGTTCAGGAGATACTTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATAAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACATTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCTTGCATGATTTT
ACCTTCTGGTTCTCAGTGAATTCAAAGCACCAGGACAACAATTCAAAAAATCTTGCTG
TAGCCTATTCTTGCTGAACATTGTTTCTTGTGGATCAATACAATACTAATAAGCTCT
TCTGTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTCATCTGTTGTGGGTGTCATCTACAACAAGGGATTTGCA
CAAGAATTTTATCTTGGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAAACCAAGTATGTTGGCTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAGAAGTTAGTGCTTGGAGAAC
TAAGGTCTTGTGCAAGAGGAGGCCCTCGCTCTGTGTTCTCGGCACCACCTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCCAGGGATGTTCTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGTCCCCTGTGTTGGATGTTAAGG**TAA**ACATAGAGAATG
GTGGATAATTACAAC TGCAACAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTAACTACTAGACAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGAACCTGTAGATAATAAGGTTAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGGTAAATGAGCTCATTACAGAAAGTGGAACATAAGAGAACAGAAGGGCAGA
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAAGAACACATTTCACCATTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTCTGTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTEFVKTVNNFVQRDTFVWDKLSVNHRTHLTKLMHTVEQATLRISQSFKTTEFD
NSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPA VVGFSAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTCTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCACTGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGC CGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCTCCCGCAGATCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA
CAAGAACGCCCGCCTGCCTGCCCGGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCAGG
GGTGTGAGTGGGTGTGTGCGGGGGCGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTGGGCACCTACCCGTGGGCCCGTAAGGCCTACTATATAAGGCTGCCGCCGGAG
CCGCCGC CGCTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGGCACGACCATCCCAACCC
GGCACTCACAGCCCCCAGCGCATCCCGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGC CGGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGCCGTGCCGGGCCCGCCCTCGCCCTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCCGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTGTGGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGAGTCGCTCTGCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCCGTCTCCCTGAGCAGTGCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTCCCTGCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTCTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAACT
GAGACCATGCCGGGCTCTTCACTGCTGCCAGGGCTGTGGTACCTGCAAGCGTGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCATTCTGCTCCCTCGA
GGTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTTAATACCTCCATCGATGGGAAC
TCACTTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTTAATTCAAGAACAGGTGATCCACTCTGA
AAACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATATCTACTTCCAGGG
ACCATTGCCCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGACAACTTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTTGAGAATAACTTGCTGTCCCAGTCACCTGC
TTCCATCTCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTTATGTCAACCTGCACTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTGCTGTGGAAAGCAGGGGGAAAGACCTAGAAC
CCTTCCCCAGCACTGGTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAATTATTTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEET
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMVPEEPEDLRGHLES
MFSSPLETDSDMPFGLVGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAACGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCCGGGAAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCCTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACACTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCTCTTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAATGAGTCAGTGGCTACGCCTGTAATCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGGATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRILGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNISGIIAAVVVA
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAACATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACATCTACATACACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTGACAAATGCAAGCATCTTCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGTGAAGGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCTAGCTATCCTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCTACAGACTAACAAATTGAAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCTTCTGTGTACCTAGAGGAAACAAACTACTGA
ACTGCCTGAAAAATGTCGTCGAACGTGAGCAACTACAAGAACTCTATATTAACTACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGAGATGATCAACAGTAAGTGGTTGATGCTCTTCCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACATTAAAGCCTTTATCA
ATCTTCGCAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCGATAACGCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT
TGCTCTCAAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTAAAAGAGTTGGGATAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAAATAGAAC
TACTAACACCTAGATTGTCTACATTCAACCCATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATGAGTCTG
CCAAACCTCAAGGAAATCAGCATAACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG
GATGAACATGAACAAACCAACATTGATTGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAGAATGTTGGCAAGTGCATTCAAGGACATGATGGAAATTGT
CTCCCTCTTATAGCTCCTGAGAGCTTCTTCTAATCTAAATGTAGAAGCTGGAGCTATGT
TTCCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAATGGCGTAACCTCCAAAGAAGGGGTTATATACCTGTATAGCAACTAACCTAGT
TGGCGCTGACTGAAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCAATTCACTGTTGGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGCTTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTGATAAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKTELPEKCLSELNLQELYINHNLLSTISPGAFIGLHNLLRLHNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFDDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIRFMEPDSDLFCVDPPFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVT KGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDGGHSYVRNYLQKPTFALGELYPLIN
LWEAGKEKSTS LKVKA TVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGTATTATGCTGACATTCCAGC**ATGAATCT**
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGT**TAGTGT**CCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTGAAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAGCTTAACCTGAACCATTGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQS FVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGR PFL
NAANDADLCNLPKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGAACGAAGGCAGCGCCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCATTCTCCTGCTGGTGTCT
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGTCTTGAGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCTGCTGGACCTAGGCAAGAACCGCATCAAACGCTCAACCAGGACAGTTGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGGCCGTGGAGGCCGGCG
CCTTCAACAACCTCTCAACCTCGGACGCTGGGTCTCCGCAGCAACGCCCTGAAGCTCATC
CCGCTAGGCGTCTCACTGGCTCAGAACCTGACCAAGCAGGACATCAGCGAGAACAAAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCAGCCTCAGCGGCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCATCCCCACCGAGGCGTGTCCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTGGACACCATGACACCCAAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACACTGGCCGTCCGCCACCTAGTCTATCTCCGTTCTCAACCTCTTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGGCCTCAACTACCTGCGCTGCTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCTGTGGTGTCCGG
CGCCGCTGGCGCTCAACTTCAACCGGCAGCAGCCCACGTGCGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTT
GTGTGCCGGGCCATGGCGACCCGCCATCCTCTGGCTCTCACCTGGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATGCCAACAA
GACCTTCGCTTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGGCCACTG
TGCCTTCCCTCGACATCAAGACCTCATCATGCCACCCATGGCTCATCTCTTTC
CTGGCGTCGCTCTTCTGCTGGTGTGTTCTCTGGAGCCGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCCCGCAAGTTCAACATGAAGATGATAGAGGCCGGGGCGGGGGCAGGGACCCCG
GGCGCCGGGAGGGGAAGGGGCTGGCGCACCTGCTCACTCTCCAGTCCTCCACCTC
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCCGCTCCCTGCTGCCCG
CCAGCCCTCACCACTGCCCTCTTCTACAGGACCTCAGAACGCCAGACCTGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPETRLLDLGKNRIKTLNQDEFASFPHLEEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTTLEESVFHSVGNIETLILDSNPLA
CDCRLLWVFRWRRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLERVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACCGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGCCGGGAAGCGCGATGGGGGCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTCGCCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACCCATCATCACTGGTT
ATAAACTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACCTCACGGAGAACCAACCCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCCTGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTAGGGGCCCTGCCACTCCTGC
GCCCCCAAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWTSDETVVAGGTVVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGGCTGCTTGGATTCTGTT
GCTGGAGACGTCTCTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCGACTTCCCAGTTACCATTATTCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCACTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTGGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAAGAGACCTTGTGCTCTGGACCCCTGCAAACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCGAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCAGTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTCGCGGGCTGCAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACACTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGCTCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCGAGTTAACCTCATCCAGA
TAGACCTCCACGGAAACCCCTGGAGTGCCTGCACAATTGTGCCCTTCAAGCAGTGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGCGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTCACCGTGGTGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTCCTACTGGACAATGGGCTTACAACGCAGATGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTTAAGACCCCAACCCAAATAGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCTCGCCCTGGCCCCGGGCTGTGGGGTTGGATGCCGGTTCTATAC
ATATATACATATATCCACATCTATAGAGAGATAGATATCTATTCTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTVGVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKIKSFRQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLLEVLIILNDNLISTILPANVFQYVPITHLDLRG
NRLKTL PYEEVLEQIPIGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDILNETTEQDLCPLKNRVDSSLPPAPPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCNNRNVSSLADLK
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNALIQLILPGTFNAMPKLRILILNNNNLLRSLPVDFAGVSL
SKLSLHN NYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPKQWAERLGSEVLMSDLKC
ETPVNFFRKDFM LLSDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLL VFTSAFTVVGMLV FILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGTGCGGCCCTAACGGAAACTGTTGGC
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGTCCGTCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCCTGGGCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCTCCTGGCAGCGCTCTGGCCCTGGGGCCTGCTACAGCCTGC
CGGCGAACACCCCAC TGCGACCGTGCTGGCTGCTCGGCCCTGGGGCAGGCGCTCAG
ACCA CGCT ACCATGAAGCGGCAGCGGCCGAGGAGGCGCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTGCACTGGAGCGCAGGCGTTCCACT
GCACCCTGGAGAACGAGCCTTGC GGTTCTCCTGGCTGTCCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCAACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTCAAGTACCAAGTTGAGGTCTGTGTCCTGCGCCGCCCCGGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCAGCTGACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTGCGCTCTGGGACAGCTCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGGCCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCCCC
GGGAGGTACCTCCGTCTGGCAAATGCGCAGAGCTCCCTAACTGCGCTAGACGACTTGGGAGG
CTTGCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCGCTCTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGGGGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCACTAACATCTATTCCCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCCCTGCCACTCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTCATATTGTGAGCACAGCAGTAGTAGTGTGGTGTGATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCACGAAAGCCCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCCTGGAGAGGTGATCTGAGGCCGCTGCTTGGCTC
CAGTCTGCACATTGCAAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTGCTGGGGAGTCCCTCTTGCTCTAGTGATGCA**TAGGAAACAGGGGA**
CATGGGCACTCTGTGAACAGTTTTCACTTTGATGAAACAGGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATGAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTAACTGGGGGACGGGTAGTGCTGGGGAGAGATTTCTATGTTATTGGAGAA
TTTGGAGAAGTGATTGAACCTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCAIDEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGGTGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGACCATAATGCCTTAAAGTGCCTCCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGGTGAGAGGGAGCGCGCGGGCAGCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCCGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGCGCGCGCGCGTGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGCGAACGCCTGGCGCCACTCTGCGCTGCGTGGCTGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGAAAATCA
CAGTTCCCAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCG
CTTCTGTGGACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAAGTGGCCAGACGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGCTGAGAGAAATGAACCTTATTCACT
TTTATCAGACTTAAGTTAAC TGCAAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACAGAACAGCCTGTCACCACCATCCCTGTAACCACGGTTAAA
ACCCACCGTGGCCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGAATTGTTATTAGCCGGACTGTTATCACAAACCATCACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCCTCTCCTCAGAACAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGCGAGGCAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATAGAACGCTCTGGATGCCCTAAAAATAAGCAATG
TAAACAGTGAACGTGTCCTTAAGCTGTATTCTGCCATTGCCATTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT
TGCCCTGCTGTCAAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCCTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTAGAAGTGCATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCCTTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCAGTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCACCTCCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTACACTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTGGAG
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCCCTGGGGAACAGAGAGAGGCCCTGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTCGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCTATGAGTGCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTTGAGTGAGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAACGGCGACTTGGTGGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA
ATCGCGGCCACCACTGTAGGACCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGAGGTAAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCACTGCCAGTTCTGT
TCTGTGTTACCCACATCCCCACACCCATTGCCACTTATTATTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCPGTERPCGGYGCCEGEGTRGGSGHCDCQAG
YGGECACGQCGLGYFEAERNASHLVCASFAGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAKGDLVFTAIFIGAVAAMTGYWLRSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTCGGGCAGCTGCAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGAGGCCGTGCTGCCGTCTCCAGG
AGCCGGTCCCCAAGGCCCGCGCTGCACAGGCACGGCGGCTGTCCCCGCGCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTCGACGTGACCGAGGGCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCGCTGCTACAGGTGTCGGTGAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGGCCCGGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTCTGGGCCTCGACAGTCATGCCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACAGGAGAGCTG
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTCTATTCTATTACTGCACATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTGTCCCTGTCAC
TGGATCTGGCTAAAGTCCTCCACCACACTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRLQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRILPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACACTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCAAAAGCACCCGTGCCTTCAGCAACTCTCCTATGTCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCTGATTCTCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACCGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAAATAGGTATCTTGAGCTTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGGCCTTCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTGCTGCCCTGCTCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGAGCTCTGTTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAACGGCTGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCCGATCACCTGAGGTCGGAGTCGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTCATGCCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAIIILCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNFGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGAGGGACAGCTGAGCGGCCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTCCACCCGACCTCTGCCCAAGGCCGAGGCCAGCTCAG
GCTCGTCCCACCCACCAAGTCCAGTGCAGCACCAGTGGCTTATGCGTCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCAGCGACGAGCTGGCTGTGAAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCTGAGGAACAAGCAACTTGCACCCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLEAAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACAGCGTCCGGTCTCGCTCGCCAGCGCGGGCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAAGGAAGGAAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAACGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCGTCT
GCCACCCGGCCTTGTGAGCGTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGGCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGTTGAGTGCCTTAGGCCCGGGTACATGGCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGGCCCGAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCTGCTCGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAAATTCCCAAAGTGTCTGAAGTGTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGGTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTGTGACACAGACTGATTAAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKGATKRLCLKHFNGLTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASNDPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACCGCGTCCGCTCCGCCCTCCCCCGCCTCCCGTGCCTCGTCGGTGGCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTGCACGCCCTGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCGGGAAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGTGGCTGCCAGCCAGTCAGTCTGCCGGGAGGGACACAGAGGCCTTGT
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCAGTCTGCCGGGAGGGACACAGAGGCCTTGT
TAAAGTCATTACTTCATGATACTTCTCGAACAGACTGAACCTTGAGGAAGCAAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCAGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT
CACAAATTAGGAACTGGTATGGATGAGCCGTCCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCAATTGCAAATATTCTGATGAGAACACCAGCAGTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCCTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCCTCTCCTCCTCTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCTAACAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAACATTCAATTCCAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGGGAAATGAAATATATG
GTTATTAGGACATATAAAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACAGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACAGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAACTTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTTGGAAAACACCTCTGTTTCTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIENLLPSDGDFWIGLRRREEQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLL
VTTVVVCWWVICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPESEGFVTLVSVESGFVTNDIYEFPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCC CGGGACTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTT CAGCATGCGCTTGTGGACCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACCGGGCTGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATT CAGAAGTCTTGTATCCAACTACCAAAGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGATACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATT CCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACTT TACCA GAGC ACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCA CGGG AAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSMPLKRFARMIEQRRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTTGGGACCTCCTTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTGATCCTT
GCCATTGCAACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGAAAGTCCCTCTCCCTCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCACAGATTTGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT
CAAECTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTCTCTGAAGAACCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCAGASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGCGACCGGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGTGCGCGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCGGAATGGTGGGCCCTAGAACAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGGCCAGGATGTTCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTVDVKRMETNYFGPVALTKALLPSMIKRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLA AVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGGATGAAATTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTG
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTTCCTGCAATGACGAAGAATAACCATTGCCATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTGGTCCCCTTACTGGTTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAACACATG
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAAGAAAAACTAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAGCACCTAGTTCTGAAAACTGATTTACCAAGGTTAGGTTGATGTCACTA
ATAGTGCAGAATTAAATGTTGAACTTCTGTTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTACTACCACTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTAAAGGAAATGAAGAAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTTGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATATTATTGATTGCACCTAAATTGTT
ATAATTGTTGTTCTTTCTGTTCTACATAAAACTGAAACTTCAAGCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTCACAATGAATATCATGAACTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCCAATGCCAAACATTCT
GCACAGGGAAAGCTAGAGGTGGATACACGTGTGCAAGTAAAAGCATCACTGGGATTAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTVVDCSNREDIYSSAKKVAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACCGCTCCGGACGCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCAGCTGCCTGGCCCTGTGAGAGAATGGTTGGTGCCTGTGGAAGGTGATTG
TTTCGCTGGT CCTGTTGATGCCTGGCCCTGTGATGGCTGTTCGCTCCCTATACAGAAAGT
GTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATAAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCTTATGTTGTACAAAGTAACATGA
CCTTGCCTGACAGAGACTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTTATAACAGTGCACTAATTCAGTTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACCGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGTTAAC
AAGTGATCCTCTTACTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACCGAACCTGAGGATCAGCTTACTATGTGAAATTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACGCCATGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTACATCCGGCAAGCGGGTGAATTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTACCCCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGGATCCTTATGTTGATAAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCATCAATAAAAATTATCCTGAAACAAGTGAGC
TTTGTTTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTAGGGTCTTGAATAGGAAGTTAATTCTTCAAGAGTAAGTGAAGGTGAGCTTGC
TAACAAACAAAGCTGTAACATCTTCTGCCATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL
VGPPFPGLNMKSYAGFLTVDNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAATCCCAGTCTTGTGGCTACAACAT
TTTCCCTTCTAACAGTTCAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCTAACAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGTAGGATAGGAAAGACTGGGTTAGTCCTAACATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTAAACCTCTGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA
GAAAACAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGACCCCTGGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG
ACAGCCGCTCTGTGGCTCTCAGGGTCTGGGTCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTTCACTCTGAGAATCGTGACTGGACCTTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTTTCATCCTGGTGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTCGGCTGCACCCGGG
CGGGTGGAAATACGGCCTCTGAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCC
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCTCTCCATCTCTCAAAGGGAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCTCCATCCGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTCACGAAGGCGCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTAACGGCTACAGCGTGGTTTTG
TGGGACTAAGAGTGGCAAGCTGAAAAGGTAAAGAGTCTATGAGTCAGATGCTCAAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTCTTGAAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTTCTTGGGAACAAAGGTGAAATGGGGAGGTAAAGAAGGGGTTAATTGTG
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNFWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNVNKLIIIDYSENRLLAGSL
YQGVCKLLRLDDLFIILVEPSHKKEHYLSSVNKTGTMGYVIVRSEGEGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRGVEYRLLQAAYLAKP
GDSLQAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWLLGKDVKQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFGTKSGKLKKVRVYEFRCSNAIHLLSKESSLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCCTCCCGCGCGGGCTGAGTGCAGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGA**TGACCA**
CGTGGAGCCTCCGGCGGAGGGCCGGCCCACGCTGGACTCCTGCTGGTCGCTTGGGTTCCCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTGCGGCTCCCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGGCTCCATCCACTATTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCTGTGGCTTGAACACCCCTACCCACCTATGTCCTGGAACTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGAACCTGGACCTGGAGGCCCTCGATGGCCAGAGATCG
GGCTGTGGGTGATTCTCGTCCAGGGCCCTACATCTGAGTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTACCGAAGCAGTGGACCTTATTTGACCAC
TGATGTCAGGGTGGTGCACCTCCAGTACAAGCGTGGGGACCTATCATTGGCTGAGGTGGAGAATGAATATG
GTT CCTATAATAAGACCCGCATACATGCCCTACGTCAAGAAGGCAC TGGAGGACCGTGGCATTGTGAACTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGATTGTCCAGGGAGTCTGGCCACCATCAACTTGCAGT
CAACACAGGAGCTGAGCTACTGACCAACCTTCTCTAACGTCCAGGGACTCAGCCCAAGATGGTGTGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGGAGGGCCCTCACAAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTCACGGAGGACCAACTTGGCTTATGAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGACAGAACGCCGGCG
ATTACACGGCCAAGTACATGAAGCTCGAGACTCTCGGCTCCATCTCAGGCATCCCTCCCTCCCCACCTG
ACCTCTTCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGCTCTGTGGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGATGGGGCAGG
TGTTTGTGAACACAGTATCAGTGGACTACAAGACAACGAAGATTGCTGTGTCAGAACGCCGGTT
ACACCGTGTGAGGATCTGGTGGAGATCGTGGCGAGTCAGCTATGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGGCTGGACAAATGGNGTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG
GTAGCTTGTCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
TCAATGGCCAGAACCTTGGAGCTTACTGGAACATTGGACCCAGAAGACGCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTACCTGTTTGAGGAGAGCATGGGGGGCCCTGATCACAGTTACGGAAACCCCC
ACCTGGCAGGAACCAAGTACATTAAGT**GAGCGGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCGCCTC**
CTCTTGACCTGAAGCCTGGCTGCTGCCACCCCTCAGTCACGAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAAACCTAAGCCTGAGGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTTGATGATGGCTTCTACAGCCCTGCTCTGTGCGAGGCTGTGGCTGTCTAGGGTGGGAGC
AGCTAATCAGATGCCACGCCAGCTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTGACGGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGTCTTGTGTTCTGGGAGGCTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCACCACTGTAGACGGTGGGGAGGGGTGTCTACCTGAGCTGACTTGT
CTTCCTTACAACCTTCTGAGCTTCTGGATTCTGGAAGGAACCTGGCGTGAAGAACATGTGACTTCCCTT
TCCCTCCCACTCGTGCTCCCACAGGGTGACAGGCTGGCTGGAGAACAGAACCTGCACATCCCTGCGTCTTCC
CAAGTTAGCAGGTGTCTGGTGTGTCAGTGAGGAGGACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGACATCC
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGG
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGGAGGAGG
ACAGAACGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCAGAACAGCAGGGCAGAGCAGGCCCTCCTTC
GAAGTGTGTCAGTCCGATTGAGCCTTGTCTGGGCCCAGGCCAACACCTGGCTTGGCTCACTGCTG
GTTGCAAGTAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PARTLGLLLL VV LGFLV LRR LDW STLVPL RL RHQ LQAK GWN F MLED STFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEA VDLYFDHLM SRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIV ELLTSDNKDG LSKGIVQGV LAT
INLQSTHELQ LTTFLFNVQGTQPKMVMEYWTGFDSWGGPHNILD SSEVLKT VSAIVDAGS
SINLYMFHG GTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTA KYM KLRDFF GSIS GIP
LPPP P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N Q S F G Y I L Y E
TSITSSGILSGHVHD RGQVFVN TVSIGFLDYKTTKIAVPLI QGYTVL RIL VENRGRV NYGEN
IDDQRKGLIGNLYLN D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTLYLP GPWLSSG I N Q V I V F E E T M A G P A
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGGCCCCAGGACCTCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGAAACGCC**ATGGCTCCC**
AAGAAGCTGCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTGTAAGGGTCATGACCGGTTCTCTTAGACGGGGCC
CGTCCGCTATGTGCTGGCAGCCTGCACTACTTCGGTACCGCGGTGCTTGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGAG
TGGGAGATGGGGGTCTCCATCCTGGTGTGCTTCGAAAACCTGAAATTCAAGAACCTC
AGATCCAGACTCCTGCCGAGTGGACTCCTGGTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTTATCACAAATGGGGCAACATCATTAGCATTCAAGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCAGTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTCTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCTGCTT
CGGAAGTATGAACCCATGGGCATTGGTAAACACTCTGAGACTACACAGGCTGGCTGGATTA
CTGGGGCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGACCCACACCTAACGTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTCTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGTGCTTGGCCCCGTGGCCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGGAAACTGGGTCCAACACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCTAACAGCAGTGAATTCAAGGGCTGTGAAGCCACCAATTCTG
GGGCAAACAACTCTAACCGAGTGGATGATGTTCCCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCTCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGTGACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACT**TGAAAGGTAGGCCGGCATGGTGGCTCATGC**
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACACCTCCACTAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACCTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCTTACATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTCTGGTTATTCAAGGATACCTTGAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTTCCCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAAACTAGGGAAATTAGTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTCACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCTGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTTGCTAAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGGCGCACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACATTACAGGAACGGAT
TTAAAGTCCAATAAACATTGCAAAATTGAGGAATCATCAGTTCCAGCATTAAAACGACT
GACTGTGTTAAAATTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTTATTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT
AGTTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCAATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCTGCCAGGCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTAAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTTAAGTCATTCACTTCCAAATCATTCTTTCTTTGGGG
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRHISRNAQDKQELHLFMLSG
VPDAVFDLTLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCAAGGGTCCGGCCTTCCTCTGGACTTGCATTCCATTCCTTTCATTGACAAACTGACTTTTTATTTCT
TTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTTCCTCCCTGACATTGGCATGGCTTAGTGGTGTGTTGGGAGGGAGACACGTGG
GCTCAGTGCTTGCACCTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGTATCCTGGCGCCTGCTCCTGCTGATAGTGTGCTGCTGTCTTACTTCAAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAATACAACCCAGACAAGGTGTGGTGGCCAAG
AACAGCCAGGCCAAAACCATGCCACGGAGTCTGTGCTGCCCTGAGTGTGAAGGATATAGAATGTGTGCC
AGTTTGTATCCCTGCCACCTTGCTGCGACATAATGAGGGCCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTGAGGCCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCTGGAACAGCTGCTGGAGATCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCCAGGAAGGGAGTTGGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAACCAAGTCA
CACAGCTGCTTATTCACACAAATCTACCCCTGCGTGGCTGGAACGTACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGTCGCCAGGCCCTGCCAAAATGGAGCTTGT
AGAAGGCTATGCCATTGACCCCTCTTAATTCTCCTGTTGGCGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCAGGGGTGCCAATATGGCAGAGACCCACAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAAGACCAGAAAACAAAGCATCAGAATTATCTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTGAAAGTAAAACATTAAAGTCTTGACGGAACCTCCAGCAATGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTGTCTTCTACTACTTCTTCTCTCTAACATCTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTGGAGGATCCTTCAACAGCCCAATTACCCAAAGCCGATCCTGAGCTGGTTAT
TGTGTGTCGACATACAAGTGGAGAAGATTACAAGATAAAACTAAACTTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTCAAATTGATTCTTCTGCATCTATGATGGCCCTCCACCAACTCTGGCTGATGGACAAGTCTGT
GGCGTGTGACTCCCACCTCGAATCGTCAACTCTCTGACTGTCGTGTTGCTACAGATTATGCCAATTCT
TACCGGGATTCTGCTTCTAACCTCAATTATGAGCAGAAAACATCAACACTACATCTTAACTTGCTCTCT
GACAGGATGAGAGTTATTATAAGCAAATCTACCTAGAGGTTAACTCTAAATGGGAAATAACTTGCAACTAAA
GACCCAACTGCAGACCAAAATTCTAAATGTTGGAATTTCCTGTCCTCTTAAATGGATGTTGACAAATCAGA
AAGGTAAGATCAGTCATTACTACCAATATAATCACCCTTCTGCATCCTCAACTCTGAAGTGTGACCC
CGTCAGAAACAACCTCCAGATTATTGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATATAACACCCAGCATGGCTTTTGAATCCAATTCA
TTGAAAAGACTATACTTGAAATCACCATTATGTTGAACTCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTTCTGATACTGTAGAGCCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTAATGCCCTAAATTCTTGAGAAGTATGAGCTCTGTGATCTGCAGTGTAAAGTTGATATGTGAT
AGCAGTGACCACCACTCGCTGCAATCAAGGTGTGCTCCAGAAGCAAACGAGACATTCTTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATGAAAGTGGCAATTAGGATTCAGCAGCAT
GAAACACATGCGGAAGAAACTCCAAACCAAGCCTTCAACAGTGTGCACTGTGTTCTCATGGTTCTAGCTG
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTGAAATCAACGGGCAGACTACAATACAGAAGCTG
CAGAACTATTAACTAACAGGTCAAACCTAAGTGAGACATGTTCTCAGGATGCCAAAGGAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGAACACACAGGCCCTGCATGAAAAAAA

FIGURE 70

MELVRLMPLTLLILSCLAEALTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLQVC SKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVRSKRD ISSYKWTDSIIGPIRLKDRSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVT VATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCGAGGAGCTCCCCAGGCTCGCGTCCCGTTGCTGCTGTTGCTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCAGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAAGTCGGCATCTTCATCCACTG
GGGAGTGTGTTCCGTGCCAGCTCGTAGCGAGTGGTTCTGGTGGTATTGGCAAAGGAAA
AGATAACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTTTAATGCCAACAGTGGGCAGATATTTCAGGC
CTCTGGTGCCAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTTGTTGGGGT
CAGAATATTCTGTGGAACCTGGAAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCGTTGGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTTCTGAGGATGAATCCAGTTCACTCCATAAGCGGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGGCTTCTATACTGCAGTGATCGTTATAACCCAGGACATCTTGCCA
CATAAATGGAAAAGCTGCATGACAATAGACAAACTGCTCTGGGCTATAGGAGGAAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACGGATAAGAAAATTATTGGCAGTTGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCAGTGCACCTTGCCTAAAGTC
TCTTCACATTGATTGTTCCATGTGTACTCAGAGGTGAGAATTCTTACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAAGTAAAATTGTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAT
TTTTTTTGCCAAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATGGTCACCTGTATAGGGCACTTACCCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCAATTATAAACTAACATAAGTGTACTGTAACCTTACAAACGTTTAATT
TTTAAACCTTTGGCTCTTGTAAACACTAGCTAAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWKKEKIPKYVEFMKDNYPPSFKYEDGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGGTGTTCCTGGCTCTGAAGGGTAGGCACGGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTGCAGAAGAGCT
TTCCATCCAGGTGTCACTGCAGAATTATGGGATCACCCCTGTAGGCTGCTGGACTAAGTTGGCGAAG
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGTGGAGA
TGGATTCTGGTCACTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTTGGTG
TCCTGATTGGAAGGTTCCAGTGGCCAGCTTGAGCCTATTGTTACAACACTCATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCACAAAGATCCATATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCACTGAGCTACACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCTGCTCCAGCTTCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGAAACTAGCACCAGTCTACAGAAAC
TGAACCATTGTTGAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCAAGAGTCAAGCAGAAACTACCGTGCATGCCTGGAA
GCTGAAGTTAGTGAGACAGAAATGAGGAGACACACTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAGAAGAAAGTCCACCCCTT
GGTCTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCACCTCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACGGAGAAAGGAGTTTGCAAAAGTCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGCTCTGAGCCGGTA
AGAGCAGAAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTGAG
ACCTAATCTCTGAAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCTCA
GTTTGATATTCTAGCTTATCTACTTCAAACCTAATTCTTATTGCTGAGACTAATCTT
ATTCACTTCTCTAAATATGGCAACCATTATAACCTTAATTATTAAACACACTAAGAAG
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGTGCCTTAACAAATGTACTCA
GCCCTCCTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTGACAAAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTAACCTACCTCTGTCGCCCTGCTCTGCTGCCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGAGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAAGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACACAGTGTCA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCATTGGCAGTGCTTCTCCTGTCATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTTCAAGCTGGTCAGTGTGTTACTGCTTATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTGACACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCCAAGGACTCTGCTTCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGCCTAAGGAGAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPLSRWLAQPYYLLSALLSAAFLLVRKLPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCCGAGAGCTCTAGCCGTCAGGGAGCTGCCTGGGACGTTGCCCTGG
GGGCCCTAGCCTGGCCGGGTACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTACGGCAAAGACCTCCTTAATGGAGTGAAAGCTGG
TGGTGGAGACACCCGAGGGAGACCCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCAGCGCGTGTGCGTGTCAAATGGTGAAGCT
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGGGGGTGTGGTCTTCCATTACAGTCCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTTCCGGGCTGGAGGGAGGGCCTGGACTGGTGAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC
AGCTTTGCCCTGGAAGTCCATGGCTGGACCGCTGCCAGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTTACCCGATCCTAACTGTGGCCCCCAGAGCCTGGG
CCGAAGCTTGCTTCCCGACCCGAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGATCCCTCACTGGCTGTGTTATTGAGTGGTT
CGTTTCCCTGTGGTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGTAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCCATTGCGGTTTGTGGCTTCTG
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGGCCAGAGTGGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGGGACAGTCTCCCTGCCCT
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGAAAGGAAAGAAACTCCCTCCCCGTTCCCT
TCCCTCTCGGTTCAAAGAATCTGTTGTTGTCATTGTTCTCCTGTTCCCTGTGTT
GGAGGGGCCCTCAGGTGTGTACTTGACAATAATGGTGTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCAGAGGATCCCTGACGCCTCTGTCCTGTTCTTGCGCTCCCAG
CCTGTCTGTCGTCGTTGGCCCGCCCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCGCCAGGGCGCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTCCTCTCCTCTGCGCCGCCGGGATCCGAAGGGTGCGGGCTCT
GAGGAGGTGACGCCGGGCCTCCCGCACCTGCCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCAACC**ATGTC**CGCAGCCTGGATCCCGCTCTGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGCGGGCAGCAGGGAGCCGCTCCATTGCTATCACATG
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTATGGGAACATAGTATATGCTTCTGTATCAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACAGACTATAGCCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACTAAAGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAACAGACTAAAGAAAACACCCGAGAAGAAAACGG
CAATAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAACATTTACAGAAGAATTGGGAAAGTGGCTCTAATGTTGGAAATTGGAAACA
GAAGGACCACATGTGGGCCCTGTTCAAGCCAGTGAACATCCAAATAGAATTACTGAA
AAACTTACATCAGCCAAGATGTTGTTGCATAAAGGAAGTAGGTTTAGAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTTAGGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACACATGCCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTTGCAAGACCTGTTATAACT
CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCC
ATGCTGAAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCTTAGTAATTGTCACAGATGGCAGTCTATGATGATGTCAGGCTTGAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTCACAAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTAGAATCCCAGCAAT
AATGGTAACATTGACAACAGAAAGAAAAAGTACAAGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTACTGACATACTAGAATCAGATAACAAACTATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGTTACAATTACAGTGT
ACTTGTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPPEKKTGNKDCKADIAFLIDGSFNIQQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCCTCCGCACCCGGCCCACCGGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCTCCGGGGAGCGAGCAGATCCAGTCGGGCCCGCAGCGAACTCGGTCCAGTCG
GGCGGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTGGGCCACCTGCTGTGCCTGC
TGCTGGCGGGCGGCGTCCCCACGGCCCCCGCCGCTCGACGGCAGCTCGCTCCAGTC
AAGCCGGCCCGCTCTCAGCTACCGCAGGAGGCCACCTCAATGAGATGTTCCGCGA
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT
CACAAATGAGACCAACACAGACAGAACAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC
ATGTAUTGCCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCCAGAGAGGCCCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTTGCCATGACCCGCCAGCCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTTCACTGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCTGCCGTGCCGCT
GCACTGCTGGAGGGAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTCTACA
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCCTACCTCTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGAGGGGTATTGTTCTCTCGTCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAAGCAGCTTCA
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACAGCCTGGTGCACCAA
AAGTGTCCCCAAAGGAAGGAGATGGGATTGTTCTTGAGGCATGCACATCTGAAATTAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAATCAGTGTGAAACATGGTT
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTCACTCCAGAGTTCTTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFGSRDQDGEILLPREVPDEYEV
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAGAGGTAAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCCTCCACTCTCCCTCCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGCAGGCCATTACCTCTGCAGCTCTTGGCTTGAGTCAGGAAACATGGGAGGG
CCAGGCACGGTCACTCACACCTGTAATCCCAGCATTTGGAGACCGAGGTGAGCAGATCAGTGGAGGTCAAGGAG
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTCTGCAACCTCTTAACCTGCACTCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GCCCCCGTGCAGATCCGGCCCTGGTATACGCCCCGCTCGTACCCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCTTGACGGCAGTCCCCCGGCACTCCCGCAGGCACACAGACCCCTGCTCTGCAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCAGGAAACAGCTTTCGGA
TGCCCCGAGACTGTGATTTCATGCCCTGCCCCAGCTGCTGAGCCTGACACCTAGAGGAGAACCCAGCTGAC
GGAGGACCCAGCTTGCAGGGCTGGCAGCCTACAGGAACCTATCTCAACCAACCAACCAGCTTACCGCATTGC
CCCCAGGGCCTTCTGGCCTCAGCAACTTGCTGCGGCTGACCTCAACTCCAAACCTCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGCAACAAAGGTAGATGCCATCTGGACAT
GAACATTCCGGCCCTGGCCAACCTGGCTAGCAGGATCTGGAGGAGATCTGGACTATGC
CCTGGAGGGCTGAAACCTGGAGAGGCTCAGGAGGCTCTCTCATGACAACCTGGAGGAGCTGGCTCCATG
GGAACAGGTGCCCCGGCTCAAGTTCTAGACCTCAACAAAGAACCCGCTCCAGCGGGTAGGGCGGGGACTTTGC
CAACATGCTGCACTTAAGAGCTGGACTGAACAAACATGAGGAGCTGGCTCCATGACAAGTTGCCCTGG
GAACCTCCCCGAGCTGACCAAGCTGGACATCACAATAACCCACGGCTGCTTCACTCCACCCCGCGCCTCCA
CCACCTGCCCCAGATGGAGACCCATGCTCAACAAACACGCTCTCAGTGCTTGCACCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAAGGAGGTAGGTCTCCACGGCAACCCATCGCTGTGACTGTGTCATCCGCTGGGCAATGC
CACGGGACCCGGTCTCGCTTCACTGAGCCCAATCCACCCGTGTCGGAGGCTCCGGACCTCCAGCGCCTCCC
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCCACGAAGCTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTCTGCAATTGCCGGACTGGCGAACCGAACCGAGATCTACTG
GGTCACCTCAGCTGGCTTCGACTGACACCTGCCATGCAGGAGGTACCGGGTGTACCCGAGGGACCC
GGAGCTGGAGGGTGAACAGCAGAAGAGGCAAGGCTATACACCTGTGTCAGGAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTTGTGGCCGTGCTCTCTCCAGCCAGGAGGACGAAGGACAGGGCTGGAGCTCCG
GGTGAGGAGACCCACCCCTATCACATCTGTGCTATCTGGTCACCCACCCAAACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCTCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCTGCTGGGAACCCACAGCTA
CAACATTACCCGGCTCTCAGGCCACGGAGTACTGGCCTGCTGCAAGTGGCTTTGCTGATGCCACACCCA
GTTGGCTTGTGATGGGCCAGGACCAAGAGGCCACTTCTGCCACAGAGCCTTACGGGATGTCCTGGCTCAT
TGCCATCCTGGCTCTCGCTGCTCTCTGGCAGCTGGCTAGCGGGCACCTTGGCACAGGCCAACCCAGGAA
GGGTGGTGGTGGAGGGCCCTCTCCCTCCAGCTGGCTTCTGGGCTGGAGTGGCCCTTCTGTCCGGTTGT
GTCTGCTCCCTCGTCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAATTCTGAAGCTAGCCTGTTCTCAGCAGTAGAGAAATCAGTGGACTACTTTTACCAA
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCAGCTGGC
CAAGACAGATGGGCTTGTGGCCCTGGGGTGTGAGCAGCTTGAAGAAAGTTGCCCTACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCCTCCATCT
CTCTCTGCCAGAGGCTCTGGGCCCTGGCTTGTGCTTCTGCTGCCCTGGCAAGGGCTGAAGGAGGCCACTCC
TCTTTCTCTGTACAGTCTCAGTTGCTTGTGCTTGTGCTGCCCTGGCAAGGGCTGAAGGAGGCCACTCC
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCTGGCTGGCATTCCGAAGCTGACTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTACACCTCCCCAACCGATTCACTCTTCTCTGTGGAGAAAATAAAAATAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANRLSLVLAGMNLREISDYALEGLQSLSFYDNQ
LARVPRRALEQVPGALKFLDLNKNPLQRVGPQDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPSSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVVVGRALLQPGRDEQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACIQAFAADAHTQACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRPLPPAWFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGGCGTGTGAGAAGGTGAAGAAAGTTCCGGACCCATGTGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC
CCTGGGCCACACTCTTCAGATCCTGGCGCTTCTACATCAGCCTAGTCATCTTACGGCCTCATCTGCATGT
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAGAACGACTTCGCGCTCATGCTGACCTCATGACCATACGACCCGCTACTCCAA
GGCGCTTCGCCGTCTTCCTGTCGGAGGTGAGTGAGAACAGCTGACGGCAGCTGAACCTCAACAAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCACGGGCCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTCCTGCCGAGAACCTGCGGGCGCTGCACATCAAGTTACCGACATCAAGGAGATCCCCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGACCTGACGGGCAACCTGAGCGGGAGAACACCGCTACATCGTCATCGA
CGGGCTGCCGGAGCTCAAACGCCCTCAAGGTGCTGCCGCTCAAGAGCAACCTAACGCAAGCTGCCACAGTGGTCA
AGATGTGGCGTGCACCTGCAAGAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCCTAACAGCCTCAA
GAAGATGGCAACCTGACTGAGCTGGAGCTGATCCGCTGCCACCTGGAGCGCATCCCCCACTCCATCTTCAGCCT
CCACAAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCCCTAACGCTGTGGTACAACCACATGCCCTACATCCCCATCCAGATGGCAACCTCACCAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTACTGCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACACCTGACCTTCTCCCTGCCGACATCGGCCCTCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTCCAGTGCAGGAGCTGACCAACCTGACGAGATCGAGTGC
GGCAACAAACGTGCTGCAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGTGC
CAACCGGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCTACTGCTCAAGCGCAGCGGCTTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG
GCCGGGCCAGCAACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGGAGGGCAGGGCTAGCTCTCCAG
AACTCCCGGACAGCCAGGACAGCCTCCGGCTGGCAGGGCCTGGGCCCTGGTGTAGTCAGGAGCAGAGCGAGA
GGACAGTATCTGGGGCTGGCCCTTTCTCCCTCTGAGAAGATCAGGCTCCCTGGGCCAGGGCAGTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGCTCCTCCCTGGAGGCCAGCTGCCCCCAGGGCTGAG
CTGCCACCAGAGGTCTGGACCCCTCATTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC
AGATAACTTATACTTCAAGAAAGTTCAGCCAGATGAAAGGTGTTCAGGGAAAGGTGGCTGCCCTTTCCCC
TTGTCTTATTAGCGATGCCGCCGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGCGAACCG
CCATGGGACGGTCACCCAGCTGGGCTCTGGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA
AAGGCCAGGCCCTGGAGCTGCCTCTCAGTTTTGTGGCAGTTTTAGTTTTGTTTTTTTAATCAAA
AAACAATTTTTAAAAAGCTTGAAAATGGATGGTTGGGTATTAAGAAAAAAACTAA
AAAAGACACTAACGGCCAGTGAGTTGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCTTCCCTGGCGCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTTGTGTTGGTTGGTTGGTGTCTTGTCTTCTTCTCCTCC
ATGTGTCCTGGCAGGCACTCATTTCTGTGGCTGCGGCCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTGGCTAATCCCGGATGAAACGGTGCCTCCATTGCACTCCCTCCTCGCCTGCCCTGCCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGGAGCCACTTCGCCAGACTTGTGTTCCCTGCCATGGGTGT
CCAGTGCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGCGCCACCTGGTCTCATGAAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGAGGTGCGGCCAGGGAGGGCAGGCAGGCTGGTTCCAAGGCCGGTTCCGTCCTGGCGC
CTGGAGGTGCACACAGCCAGTGGCAGCTGGTGGGAACCTGCTGGTGGTAACTGCTTGTCTTGTCTTAA
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCAGGTTAGAGTCCTTGTCTTAA
CCATCGTCTGTCGGTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILII CYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLDKLQRQLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELI PDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNNVLQSLPSRVGELETNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGATTATGTACGGTCCGAAGGATGCCATACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCACTGGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCACACTTGCGGGGT
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTCAAGC
CACGTGAGACACCTACAACGAGATGCCCTAACAGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTCAAATTATTCTGAGGATCAACCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCATGGTCAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAAGCTAGCTGAAGTGGAAAGGCCCTGT
ACAGTGAACCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGGACGCCAACTCGGGCGTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCCAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATACTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCACCTGTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCACATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATATAACA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTAAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPEQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGGTCCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGAGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTGGCCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGGAAAGACTCTCGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCCTCAATAACGAAAATACCTGACCCTAGAGAAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCCACACGGTGAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAACTTGACCTACAAGACGTGG
GCTCTGGCACAGCAATAACAGCCAAGCCTGTGCCAGTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAAACAGGGCCGGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGTGGTCCAACATCTCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCCTGCAGTGGCTCATGCTGTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCCCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTGGAAGACACCAGTCCGCCAACCTCCCTGCCCTCCAG
CCCCATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATCCATGGGTGTCGGAACCTCGCCCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCTGTAACAGGC
TGGGGAACACCAACTTCCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCATC
AGGAGAGATGGCTTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGAAA
TGCTGTGAGCTTGACTTCAACTCCACCCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCAAAGGGTTGTATACAGACTCTGTGCACTA
TTCACTTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTACCCTTACTCT
TTCCCTACCCCTGACATCCAGAAACAATGCCCTCCAGTGCATACTCTCAATCTTGTCTTATG
GCCCTTCCATCATAGTTGCCCACTCCCTCTACTTAGCTTCCAGGTCTTAACCTCTTG
ACTACTCTTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTTGCTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCGGCCCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGAACAGTGCTCGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTTACAGTGCCCCCTGAAACCCACTTG
GCCTGCATACCGCCTCCCTGTCGTCTGCCCAAGTCTACCCCTAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTATAAGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCTTCTAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCCTGCTAACGAGCTGCCAGGGGCCAGCGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGAGCGAAAAATTATTGGCATTTCAGG
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGAACAGTGTCCCTGGCAGCAATTAAGGTCTTACAGGATTTGAACTTCAACGTGGCTGTCAAATCACTC
AAATTGTTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTGT
CAAACTTGATTTATTCATCTGAACTTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVG
IYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTS
VKLSTGCTGT
LVAEKHVLTA
AHC
IHDGKTYVK
G
TQKLRVGFLKPKFKDGGRGAND
TSAMPEQM
KFQWIRVKRTHVPKG
WIKGNANDIGMDYD
YA
LLELKPKH
RKFMKIGVSPPAKQLPGGRIHFSGYDND
RPGNLVYRFCDV
KDETYD
LLYQQCD
AQPGASGSGVYVRM
WKRQQQKWERK
IIIGIFSGH
QWVDMNGSPQDFNV
AVRITPLKYA
QICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCC**ATGGTGGTT**
CTGGAGCGCCCCCAGCCTGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGAAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGTGGCTGGTGGAGC
CCCACCCCTGTATTCCCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCCATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCCCTATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGAACAGGCC
GGGGTCTACATCAGCCTCTTGCGCACCCTCAGGGCAGGCCAGGGCTCTGGGGCCG
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCAGGCCAGGGCTCTGGGGCCG
CCGGCGCTCT**AGGGCGCAGCGGGACCGCGGGCTGGATCTGAAAGGCGGCCAGATCCACA**
TCTGGATCTGGATCTGGCGGGCTCGGCGGTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTCCGGCCCCGCCGGAGCGCTTTGTGTATATAATGTTAATGATTATTAT
AGGTATTGTAACCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRQKVGVAV
WVEPHPVYSWKEGACADIALVRRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 100

MHGSCSFLLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDVPLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPyQEGTPCSQCPSGYHCKNSLCEPIGSPEDAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPPSMATEAPPCTEVPSILAHLPSLDEEPVTFPKSTHVPIPKSADKVTDKTKVPSRSPENSBDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVVSGLNNSPGHVGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTAGGCTTTCAATTGGGAAGCCCCCAACAGAACCGTCAATTCTCCAAGTTATGGTGGACGT
ACTCTGTTCTCCCTGCTTGCCTTCACATTAGCAGACCGACTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAAGCCTCGAGAAAGTGAAACTGAACACAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGCAAATATTACACTCTCTCCCTGGCTGAAACAGGATTGTGAAATACCTCCCTGA
ACATCTGAAAGAGTTCTGAGTCCCTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGATCTCACAGCAACCGAGTCACATCAATGGAACCTGGTATTGACAA
TTTGGCCAACACACTCCTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGAAACATCTGAAACTTGAACCCAGGAAAGATTTAAAGTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAAACTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGGAAATTTCAGCTGGACCAAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGCTTGCCAGAAGCTCAG
TGAGCTGGACCTAACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTTACTAAATAC
ACTGCACATTGGAAACACAGAGTCAGCTACATTGCTGATTGCTTCCGGGGCTTCAAGTTAAAGACTTT
GGATCTGAAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAAATGCAACAATT
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACCTT
TCAGAGCTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAACGATTTTGCTGTTAGCCAGA
TGGCTTGTGTGATGATTCCAAACCCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTTTC
CAATTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGATCCCCAATGACTTTGCTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAATTATGCAACACCTCCGGGCCAAGGTGGAGGATGAGTGGAGTATACCAC
CATCCTTCGGTGGCGAGGTGGAATTGCGAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACTTTGGTTTC
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACC
CCGAGCTGGGGCCATGGCACGCTGGAGTGTGCTGCTGGGGCACCAGCCCCCAGATAGCCTGGAGAAGGA
TGGGGCCACAGACTTCCAGCTGCACCGGAGAGACGCATGTGATGCCGAGGATGACGTGTTCTTATCGT
GGATCTGAAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAGGAAATGC
AACTCTGACTGTCCTAGAAACACCATATTGGCGGCCACTGTTGGACCGAACTGTAACCAAGGAGAAAACAGC
CGTCTACAGTGCATTGCTGGAGGACGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGGGT
AACCGAGAGGCACTTTTGCGAGCAGGCAATCAGCTCTGATTGTGGACTCAGATGTCAGTGTGATGGGAA
ATACACATGTGAGATGTCTAACACCTTGGCACTGAGAGGAAACGTGCGCTCAGTGTGATCCCCACTCCAAC
CTGCACTCCCCCAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTTGGTGTGATCATAGC
CGTGGTTGCTGTGGTGGCACGTCACTCGTGTGGTGGTCACTATACACACAAGGGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCACTCAGGGAAAGTT
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAAAGCCACCAAGTTGTCACTATCTCAGGTGCTGG
ATTTTCTTACACACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC
CACAGATCTGTTCTTGTCCGTTGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGTATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCACTGACCAAGAACAGTTAATGGACCACTATGAGCCAGTTA
CATAAAGAAAAAGGAGTGCTACCATGTTCTCATCCTCAGAAGAACCTGCAACGGAGCTCAGTAATATATC
GTGGCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTAAAGTTAGTGCACATCCAGAGCCAGCGTCGGTTGCCCTGAGTAATTCTTCATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGGTAGAGGAAGATGGGAAAGAAAAGGAC
AGATTTCAGGAGAAAATCACATTGTAACCTTAAACAGACTTTAGAAAACAGACTCAGGACTCAGTC
TTATGACTGGACACA**TAG**ACTGAATGAGACCAAGGAAAAGCTTAACACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAACTTATGTTTTAAATGGAGTTATGAATTAAAAGGATAAAATGCTTATTATACAGAT
GAACCAAAATTACAAAAAGTTATGAAAATTACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA
TTTTTTAACCTTGTGTTATGCAAAAGTATCTACGTAAATTAAATGATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATACCTGCTTGTACCAATT
TTAAATAGAAGTTACTCATTATATTGCACTTATTTAATAAAATGTGTCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLHNRLSFIKASSMSHLQLSLREVKLNNNELETI PNLGPVSAN
ITLLSLAGRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLMNRNRI SAI PPKMFKL PQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGDGFWGLSNM EILQLDHNNLTEITKGWL YGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAF RGLSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRLR LILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWL PQWVAENN FQSFVNASC AHPQLLKGRS IFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDPMFTA WKDNELLHDAEMEN YAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVI SNHFGSSYSVKAKLT VNMLPSFTKTPMDLTIRAGA
MARLECAAVGH PAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDV KIEDIGVY S CTAQN
SAGSI SANATLTVLETPSFLRPLLDRVTKG ETAVLQCIAGGSPPP KLNWTKDDSP LVVTER
HFFAAGNQLLIIVDSDVSDAGKYTC EMSNTLGTERGNVRLS V IPTPTCDSPQM TAPS LDDDG
WATVGVI IA VCCVVGTSLVWVVIYHTRRRNEDCSITNTDET NLPADIPSYLSSQGT LAD
RQDG YVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATD LFLCPFLGSTGP
MYLKGNVYGS DPFTYHTGCSPDPRTVLM DHYEPSYIKKKECYP CHPSE E S CERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFM GTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLEN Y RTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTGGTGGTGGCTGTTGGGTGCCTGCAAAATG
AAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGATAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAATGGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACAGAGTTAGACCCGGGGGGTGGTGTGACATAATAATCTTAAAGCAGCTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAAGAAAAAGTATGTCATTTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATAAATGGAAATGAAAAGTGGGGCTTTTAGTAAAGTAAGAAACT
GGTGTGGTGGTCTTCTTGAATTCCCACAGAGGAGGGAAATTAAATAATCATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAACAGCAGACAGTTGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTCTCTTCATCACACCTCTTTTTAAAT
TTTTATTCCCTTTGGTATCAAGATCATGCGTTCTCTGGTCTTAACACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTTGAATTCCAGAACGGACCAACACAGATAAAATTATGA**ATGTTGAA**AGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGC
GCTGGCTCTTCAACTCTTGTGGTGGTCTGGTCTGGCTAGACCTGCCCTCTGTGTGCTCTGCAGCAA
CCAGTTCAAGGTGATTGTGTTGGAAAAACCTGCGTGGAGGTTCCGGATGGCATCTCCACCAACACGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCCTCAAGCAGTGAGGACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGGAACCTCAACACTCTGA
ACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTGGTT
GCGAAACAACCCATTGAAAGCATCCCTTATGCTTTAACAGAAATTCTTCTTGCGCCGACTAGACTTAGG
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGCCAATTGAGGTATTGAAACCTTGC
CATGTGCAACCTCGGAAATCCCTAACCTCACACCGCTCATAAAATAGATGAGCTGGATCTTCTGGAAATCA
TTTATCTGCCATCAGGCCCTGGCTCTTCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATACTAAC
ATTACTGCCCTCATGACCTCTCACTCCCTGCACTCTAGAGCGGATACATTACATCACACCCCTGGAACCTG
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCCTGTTGTGCCGGTG
TAACACTCCTCCCAATCTAAAGGGGAGGTACATGGAGAGCTGACCCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCTAACATGGAAACAGTCATGACACATGGGGCTACAAAGTGCAGGATAGCTGT
GCTCAGTGATGGTACGTTAAATTCTAACAAATGTAACTGTGCAAGATAACAGGCTGACACATGTCATGTTCTTACTTTC
TTCCGGTGGAAACTACTGCTTCAGCCACCTGAATGTTACTGTCAGCAACACTACTCCTTCTTACTTTC
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACACAGATAACAAATGTCGGTCCCACCTCC
AGTGGTCGACTGGAGACCAACATGTGACCACCTCTCACACCCAGAGCACAGGTCGACAGAGAAAACCTT
CACCATCCCAGTGACTGATATAACACAGTGGGATCCCAGGAATTGATGAGGTCTGAGACTACAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTCAGTGATGCTGGTCTTCTAACAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCTGTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT
CAACCACACAACACAGTTAACACAATAATTCAATACACAGTTCACTGTCATGAACTGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACATCAAAAAAA
GACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVKNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPLSRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMNNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGGCTGCTCAAGCTGCAACTCTGTGCA GTTGCAGTTGGCA GTTCTTCCCTCCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGCACCGC
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTGTGCCGGGCCCGAGCGCGCGCGCGGGCTGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCGCG**ATGAGCGCGCCAGCCTCCGTGCGCGCCGCGGGCTGGAGCTGCTGTGCG**
GCGGTGCTGGGCCGCTGCCCGTCCGACAGCGGGTCCGCGGGAGACTCGGGCAGGCCCTCTGGGTAGCCGCC
GAGCGCCCAGTCCCCACTACCTCGCCTGCCCTGGGACTGCTGGACTGCAAGCAGATTCTTCATCAAGGCAAGTCC
CCCAGGCCACTCCGTCCTGGTCACTGGACTTAAGTCACAACAGATTCTTCATCAAGGCAAGTCC
ATGAGGCCACCTCAAAGCCTCGAGAAGTGAAGACTGAACACAATGAATTGGAGACCATTCCAATCTGGGACCA
GTCTGGCAAATATTACACTCTCTGGCTGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCTGAAACTTTGACCTTAGCAGCAACAATATTTCAGAGCTCAAACGTCATTCAGCCCTACAG
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTCAGCAATTGGCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAGATGTTAAACTGCCCAACTGCA
CATCTCGAATTGAAACGAAACAAGATTAAAAATGTAGATGGACTGACATTCAAGGCCCTGGTGTCTGAAAGTCT
CTGAAAATGAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGAAATTG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGAGCTGGACCT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTCTGGCTAAGCTACTAAATACACTGCACATTGGG
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTTGACAAACTGAGGGCAGTGTACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCAGTGGTTGGATGCAATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGCTTTACAAGGCAATGCAATTTCACAATGAAGAAACTGCAACAATTGCAATTAAATACA
TCAAGCCTTTGTGCCAGTGGCTAAATGGCTCCACAGTGGGGCGGAAACAACACTTCAGAGCTTGTA
AATGCCAGTTGTGCCATCTCAGTGTCTAAAGGAAGAACGATTGGCTGTTAGCCAGATGGCTTGTGTTG
GATGATTTCACCAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCAATTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGAATTCCCAATGACTTTGCTGGAAAGAACATGAAACTACTGCA
GCTGAAATGAAATTATGCAACCTCGGGCCAAGGGAGGGTGTGAGTACACCCATCCTCGGCTG
CGCGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCATTGGTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTCCCTCATTCACCAAGACCCCCATGGATCTCACCACCGAGCTGGGCC
ATGGCACGCTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCTGGAGAAGGATGGGGCACAGAC
TTCCAGCTGCACGGAGAGACGCATGATGATGCCAGGGATGACGTGTTCTTATGTGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACACTGAGGAAGTATTTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTCGCGGCCACTGTTGACCGAAGTGTGTCATCTCAATCATTGGTTCATCCTACTCTGTC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGAGTGTAGCCCATTGGTGTGTAACCGAGAGGCAC
TTTTTGCACTGGCAATCAGCTTGTGATTATTGTGGACTCAGATGTCAGTGTGATGCTGGAAATACACATGTGAG
ATGTCTAACACCCCTGGCACTGAGAGAGGAACGTGCGCTCAGTGTGATCCCCACTCCAAACCTGCGACTCCCT
CAGATGACAGCOCCTCGTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTGCTGT
GTGGTGGGACGTCACTCGTGTGGGGTGTGATCATATACACACACAAGGCGGAGGAATGAAGATTGCA
AACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTGATCTCAGGAAACGTTAGCTGACAGGCAG
GATGGGTACGTCTTCAAGAAAGTGGAAAGCCACCACTGGTACATCTCAGGTGCTGGATTTCCTTACCA
CAACATGACAGTAGTGGACCTGCCATTGACAAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTC
CTTTGTCGTTTTGGGATCCACAGGCCCTATGTATTGAGGGAAATGTGATGGCTCAGATCTTGTGAAACA
TATCATACAGGTGCACTGCTGACCAAGAACAGTTTAATGGGACCATATGAGGCCAGTTACATAAAAGAAAAAG
GAGTGTACCCATGTTCTCATCTTCAAGAAATCCTCGAACAGGAGCTCAGTAATATATCGTGGCTTCACAT
GTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAAAATCTGTC
TCTTAGATTAGTGCACAAATCCAGAGCCAGCTCGGTTGCCCTGAGTAATTCTTCATGGGTACCTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTGCA
CAGGAAAGAGCCTTTATTTGAAAGCTCATCTTCCCCAGACTGGACTCTGGGTAGAGGAAGATGGGAAAGAAAGGACAG
GAAAATCACATTGTACCTTAAACAGACTTAAAGAAACTACAGGACTCCAAATTTCAGTCTTATGACTGGAC
ACATAGACTGAATGAGACCAAAAGGAAAGCTTAACATACTACCTCAAGTGAACTTTATTAAAAGAGAGAGAAT
CTTATGTTTTAAATGGAGTTATGAATTAAAGATAAAATGCTTATTATACAGATGAACCAAATTAC
AAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAAACTTTG
TTTATGCAAAAAGTATCTACGAAATTATGATATAATCATGATTATTTATGTATTGTTATAATGCCAGA
TTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCAATTGTTAAATAGAAGTT
ACTTCATTATATTGCACTTATTTAATAAAATGTGCAATTGAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRSLFIKASSMSHLQLSLREVKLNNNELETPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLRLDDSSFLGLSLLNTLHICNNRVSYIADCAFRLSSLKTLIDLKNNEIS
WTIEDMNGAFSGLDKLRRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAPHQLLKGRSIFA VSPDGFCVDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLRTVTKGTA VLOCIAGGSPPP KLNWTKDDSP LVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLS VIPTPTCDSPQMTAPS LDDDGWA
TVGVVI IAVVCCVVGTSLVWVVI YHTRRRNEDCS ITNTDETNL PADIPS YLSSQGT LADQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGS DPFTYHTGCSPDPRTVLM DHYEPSYIKKKECYP CSHPSEES CERSFSN ISWPS
HVRKLLNTSY SHNEGPGMKNLCLNKSS LDFSANPE PASVASSNS FMGTFGK ALRRPHL DAYS
SFGQPSDCQ PRAFY LKA HSSPD LSGSE EDGKERTDF QEE NHIC TFK QTLEN YRTPN FQSY DLD
Signal sequence:
amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCCAGCTTGACTTGAATGGAAGGAGGCCAGCCTGGCTGGAGCGCAGCTGAGAC
TGGGGAGCGCGTTGGCCCTGTGGGCGCCGCTGGCGCCGGGGCGCAGCAGGGAGGGGAAGCTGTGGCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCAGGGAGAGGCCCTGGTGGTCCCGTCCCTATCCCTCCTTATATA
GAAACCTTCCACACTGGGAAGGCAGGGCGAGGAGGGCTCATGGTGGAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCAATTGGAGATTACAGATTTTACAGATAACCAAATGGAAGGCCAGGAGGGCAGAACAGCCTGCC
TCCATCAGCCCTGGGCCAGGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGGCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCCTGAGGGGCCAGGATTGGCCGAA
GTGGGCCAGCCTGAGGGCGAAGAGAACGAATTGGCAGGGAGGCCGGTGTGGTACTGAGCCCTGAGG
AGCCCCGGCCTGGCCAGCCGGTCACTGCCCGAGACTGTGCTGTGGCCAGGAGGGCGTGGACTGTG
GCGGTATTGACCTGCGTGAATTGGGGGACCTGCCTGAGCACACCAACACCTATCTCTGCAGAACAAACAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAACAAACCGC
CTTCCCGAGGGCTCCAGAGAAGGCGTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCAATAACAAGC
TGACCTTGGCACCCCGCTTCTGACCAACGCCCTGATCAGTGTGGACTTGTGCTGCCACTATCTACCAAGATCT
ATGGGCTCACCTTGGCAGAAGCCAACCTGAGGTCTGTGTAACCTGCACAAACAAGCTGGCAGACGCC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCATCTGTCAGCAACTCTGCGCACGTGC
CCAAGCACCTGCGCCTGCCGTGACAAGCTGCACCTCAAGAACAAACAAGCTGGAGAAGATCCCCCGGGG
TCAGCGAGCTGAGCAGCCTGCGCAGCTACCTGACGAGAACAAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCCAGCAACAAACCTGTCTCGGGTCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCACCTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCGAGCTGCCAGGGAGCAGGGCATCCACCCACTGGC
TCAAGCGGTTGACACGGTGCACCTGACAACACCGCCTGGAGCGCTGCCCAGTGGCCTGCCCGTGC
GCACCCATGATCCTGCACAACCAGATCACAGGCAATTGGCCGAGAAGACTTTGCCACCACTACTCC
AGCTCAACCTCAGCTAACCGCATCACAGGCCACAGGTGCACCGCAGCGCTTCCGCAAGCTGCGC
GCTCGCTGGACCTGTGCGCAGGGCTGCACACGCTGCCACCTGGCTGCTCGAAATGTCCATGTGCTG
TCAAGCGCAATGAGCTGGCTGCCAGGGGGCTGGGGCATGGCTAGCTGCGTGAAGCTGTACCTCA
CCAGCAACCGACTGCCAGGGAGGCCCTGGGCCCCCTGGCTGGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTA
AGATTAGTGCCTGGCCGCAATGCCCTCGACTCCACGCCCCAACCTCAAGGGGATCTTC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGG
TAGAGTTGGTGAACATTCAAGGACGTGGCCCTTGGGGAGGAAAGGAGGAGGAGGAAGAGGAGGAGG
AGGAAGGAAACAAGATAGTACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTCTGC
AGCACACGCCCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGC
TCCCATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCACGGGTGCTCCACGCC
ACACACATCACACCCCTCAAACACCCAGCTGCCACACACA
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAGGGCTGCCCTGCCACACACAGGC
TCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACATGCACAAGTC
CAGCCCTCAAAGCCTATGCCACAGACAGCTTGGCCAGGCCAGAATCAGGC
GTCCATCTGTCGTCGCTGCCAGGTGCTGGCCAGGTGCCACCCCT
GGAACTCACAAAGCTGGCTTTATTCTTCCATCCTATGGGGACAGGAGC
TGGCCACCCCTGCTCTCCAGGTGCTGGGAGCTCAAGAGTCCCTCC
CAGGCACTTTCCAATGGGCAAGGCCAGTGGAGGAGGGATGGGAG
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGCCAGGGAGGAAGG
GTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCC
GCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFEEEEPVVLVSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLQLQNNQLEKITYPEELSRLHRLETLNQLQNNRLTSRGLPEKAFLTNLYLYLANNK
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLIILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSIRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGGCCGCAGCAGACCTGCTCCGGCGCGCCCTCGCCGCTGTCCCTCCGGAGCGGCAG
CAGTAGCCGGCGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCTCCCCTCGCGCCACCACCC
CAACCTGTCCTCGCGCCACTCGCGCCAGGGACCCAGTGGATTTCTCTGGCGCTGGT
GCTGGTATCCTCGCTCACCTGCAGGGCGCCGAGTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCTATGTCGTTATGGTGGAGGATTGACTGCTGGGCTGGGCTCGCCAGTCTGGGGACAGTGTCA
TGTGTGCAACACGATGCAAAACATGGTGAATGTATCGGGCAAACAAGTGCAAGTGTATCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGCGCTGTAAGCACAGGTGATGAAACACTTA
CGGCAGCTACAAGTGTACTGTCACGGATATATGTCATGCCGATGGTCTGTCAGTGCCCTGACCTG
CTCCATGGCAAATGTCAGTATGGCTGTATGGTAAAGGACAAATACGGTGCAGTGCCCATCCCCGGC
GCACCTGGCTCCTGATGGAGGACCTGTAGATGTTGATGAATGTGTCAGGAAGAGCCTGGCTAGATT
TAGGCAATGTGTCAACACTTTGGGAGCTACATCTGCAAGTGTATGTCATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGTCACTTGGTCAGTATCAGTGCAGCAGCTTGCTCGATGTTATAA
CGTACGTGGGCTTACAAGTGCAGTAAAGAAGGATACCGGGTGTGACTGACTTGTGTATATCCAAA
AGTTATGATTGAAACCTTCAGGTCAAATCATGTCACAAAGGAAATGGTACCTTTAAAGGGTACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAAGTACTTGGTGGCTCGAAGACACCATATATTCTCTTATCATTACCA
CAGGCCTACTTCTAACGCAACAAAGACCTACACAAAGCCAACACCAATTCTACTCCACCAACCCACC
CCTGCCAACAGAGCTCAGAACACCTTACACCTACAACCCAGAAAGGCCAACACGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGGG
AGATGTGTTCACTGTTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACGGAAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAGCTGCACGGCTTGGCTACCTCTGGCGCCTCATGCATTAGGGGACCTGTGCCTGTCATTCA
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCACGGAGCAGCCCTGTG
GGGAAGAAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTGGCAGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGCAAACCATGATGGTTTCAGTATAAGGGGTTGGCACAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTTCTTCTAAAAAATTAGA
AAAAAATTGTCATTTAGATGGTTAAAGATGTTCTACCAAGGAAAAGTAACAAATTATAGAATTCCC
AGATGTTTGTACTAGTAGTATGCACTGAAATCTTACAAGTAAATAATTGGACAAGGCTTAATTAGG
CATTTCCCTCTTGACCTCTAATGGAGAGGGATTGAAAGGGAAAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC
AGATATTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCAAGGAACACAGTTAGAGAG
ATTTTCATGGGTGCAATTCTCTGCTTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC
ACACGGCAGACCTTCCTCACCTCATCAGTATGATTGAGTTCTCTTATCAATTGGACTCTCCAGGGTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTAACTGGTAAAGGCAGGGCTGG
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTTCA
TCCTTATGGTCATATAACTGCACAGTGAAGATGAAAGGGAAAATAATGAAAATTTCAGTTTGATGCCAA
TGATACATGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCCAAATGGCCTAATAAAACAATTATGTAATAAAACACTGTTAGTAAT

FIGURE 110

MDFILLALVLVSSLYLQAAAEDFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTEFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASSTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIREKDNDLHWEPIRDPA GGQYLTVA
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGLQVFVRKHGAHGAALWGRNGGHGWRQ
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTTCCCTTGCAACAGGTGCTGCTCGGGGCTGA
AGGTGACAGTGCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCAGATCATATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTACTGGCTCTGTGAATAAGTCTGGTCTGACTTGAATACC
AACACAAGTCACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTC
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTACATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT
GCCTGGTGAGGAACCCGTCACTGAAATGGAAGTGAATCATATTGCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAATCATTGTCACTTCTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTTGCTGGGCAAGATTGCAAGTACAGT
GTATGAAGTTATT CAGCACATCCCTGCCAGCAGCAAGACCATTCAAGTGAACTTTCATGG
GCTAAACAGTACATTGAGTGAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAACTGGAAATCAGTGAAGAACACCAGGACCAACACCTCTTACTCATTATTCTTACA
TGCAGAAATAGAGGCATTATGCAAATTGAACCTGAGGTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGCACAGGGTTCTCATAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGAGTTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTTGTATTTGACAA
CAAAGTAATAAGGATGGTGTCAACAAAACAAACTATGCCCTCTTTTTCAATCACC
AGTAGTATTGAGAACACTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTGCTTTAAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDSCADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGAAATGGCGCCCTCCGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGTGTT
GCTTGCGGTGCTCCCTGGACGCACGGCGCGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCTGCT
TGTCAAAAATCTCAACCGGAAGGAAAGTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAAGACCTTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAAATCTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAAGACAACGCTCTGGGTCCATCATTGCCACAGATAATCCTAGTTAAATTTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTACTTTTGAAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTTACAGTTGAAATATGATTAAGCACAGTATGATG
GTTTAAATAGTCTCTAATTTTGAAAATCGTGCCAGCAATAAGATTATGATATTGTATT
TTAATAATAACCTATTCAAGTCTGAGTTTGAAAATTACATTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAATTATTCCATTGATATAATTTCTCTG
TTTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTTCAGTGACAATTCGGGTCTTTAGAGGTATTCCAAAATTCCCTGT
ATTTTTAGGTTATGCAACTAATAAAACACTACTTACATTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAGTTCATGGTATTCTTGATTC
CAACAAAGTTGATTTCTCTGTATTTTCTTACTTACTATGGGTTACATTTTTATTTT
CAAATTGGATGATAATTCTTGAAACATTTTTATGTTTAGTAAACAGTATTTTTGT
GTTTCAAACTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTAAAATT
TTGGCCACTTTTCAGATTTTACATCATTCTGCTGAACTTCAACTGAAATTGTTTTT
TTTCTTTGGATGTGAAGGTGAACATTCCTGATTTTGCTGATGTGAAAAGCCTGGTA
TTTACATTGAAAAATTCAAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG
CATCTTCTTGTATATGCTTAAATGTATTTTGCTCATATACAGAAAGTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATTTTAAATAAACATTTTTTAAAAGACAA
ACTTCATATTATCCTGTTCTCCTGACTGGTAATTGTGTGGGATTTCACAGGTAAAAA
GTCAGTAGGATGGAACATTTTAGTGTATTTTTACTCTTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAATACAATGAATCACTGACCATTACGTAGAGAC
AATTCTGTAATGCCCTTCTTCTAGGCTCTGTTGCTGTGAAATCCATTAGATTTACAG
TATCGTTAATACAAGTTTCTTAAAGCCCTCCCTTAGAATTAAATATTGTACCATT
AAAGAGTTGGATGTGTAACTTGTGATGCCTTAGAAAATATCCTAAGCACAAAAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLWLGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGGGAGACCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTCTGC
ATTGCTGATGGCTGGTTGGTCTGAGCTGTGAGGCGAATTCTCACCTTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTCAGTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTGAC
TAGCAAGTCAGCTGATGCTGAGGGTACCTGGCTACCCGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTGTGAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGAGTTCTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCAGGAACCAAGTACCAAGGAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATGCAACCGTGCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGAAATCTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAACAGCTGAGCTAGCAACCCCAGAAGGCA
TCTATGAGAGGGCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG
GAGGGTGTCAAACGTACACCCCCGTAGACAGAACAGGCTTTCTGTAGGTACCAATGGCAA
CAGGGCCCCACAGCTGCTCATGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGCACA
TCGTCAGGTACTACGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATGCAAAA
CCTAAACTTGACAGGCCACCGTGTGATCCAAGACAGGAGTCTCACTGCGCAGCTA
CCGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCCGTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCATTGACTTCTCTAGGCGACCTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGGGAGGAAAGGTGACTACCGAACAGACATGCTGCC
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGACCATCCTTCTGTCTCCCTGGTC
CTTCAGCCCATGTCACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTGGAGGAAATGAATGTTGTCTGGAGCAGAGGGAGGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTCAAGCTGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGCTAGCGCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGTTACCAAAAAATAAAATGTCCTACAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSHVQAEFFTSIGHMTDLIYAEKELVQLKEYILVEEAKLSKIWSA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEATTKSQVLDLYSYAVFQLGDLHRALELTRRLSLDPHSERAGGNLR
YFEQOLLEEREKTLTNQTEAEELATPEGIYERPVYDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIYRYYDVMDSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVN

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCCTCCTCTTTAGTGGAAAGACAGACCATAATCCAGTGTGAGTGAAATTGATTGT
TTCATTATTACCGTTTGGCTGGGGTAGTCCGACACCTCACAGTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTCTGGGATGCTGGCCTGGAAGCCAGCGGGCCTGCTCTGTCTTGGCCTCATGACCC
CAGGTCTGGTAAAGCTACTACTGGCCTGGCTGCCATCAATCATTGATCCTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCAATCGACTGAGCTCCCTGTGGCTCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCCTGGGGTGAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCCTGTGAGGCTGTAGGGGAGCGAGGAGGGCACAGAACAGGAAATTGAGCTCGCTAGACCAAAGTG
ATGAAGACTCAAACCCGGATTGTCCCCTACTACAGGGACCCAAACAAGGCCATACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGACTGGCTCCCGTGGCTGGCTGGCTCTGAGCTCCCGAGCTACACTGTCCA
CTTGGCCCTGGCTGTGAACCGTACGGTGGCCATCACTTCCCCTCGGTTACTCTACTTCACTGGCAGGGGGGG
CCCAGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGATGAGCGGGGCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGCCACTACGACTGGTCTCATCATGCAGGATGACACATATGTGCAGGCC
CCCAGGCTGGCAGCCCTGCTGGCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCATG
GCGCAGGCGAGCAGGCCGGTACTGTCTGGGGCTTGGTACCTGGTACGGAGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCTGAGCTGGCTGGACGCTGCGCTATTG
ACTCTCTGGCGCTGGCTGTCTCACAGCACAGGGCAGCAGTATGCTCATTTGAACGGCCAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTCGGTTCTGAGTGCCTCGCGTGACCCCTGCTCCGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTGGAGCGGTTACAGTGAACATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGGTGGCTCCCTGCTCCCTTA
CACCAACTCTCGTTTGGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTTCTCTGTGCAGATGGGG
CTCCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCCTATCAGCCCCGCTCGCCTCCAGAACGAGCAGCAGTGCCTAACGGCTATGGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCTGGACCTGCTGGTGAATGTGACACAGCGTGGGACCGGGCCCTGGCTCGCA
GGGTCAAGCCTGCGGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGCACTGAGGCCACCCAGTGC
AGCTGGTGTGCGCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGCCATGTCC
TGGAGGCCACGAGAACATGCATTGCTCACCTGTTGGTCTACGGGCCACGAGAACAGGTGGAGCTCCAG
ACCCATTCTGGGGTGAAGGCTGCGACGGAGTTAGAGCAGCGACGGTACCCCTGGGACGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTGAAGAACGACCCCTGTGGACACTCTCT
TCTTCTTACACCGTGTGACAGGGCTGGCCGAAGTCTCAACCGCTGTGGCATGAATGCCATCTCTGGCT
GGCAGGCCCTTCTTCCAGTCCATTGCGAGGTCAATCTGCCCTGTCACCACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCCCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGCCCGAGCCCGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGCTGGAGGTGATGGATGTTTCCCTGGTCTCAGGGCTCC
ACCTCTTCCGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCACGGCTCAGTGAAG
AACTTACCAACCGCTGCCGCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGCCTAACCTATTACCTTCTTGTCTGCCCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGGACAGATAGAGAATTGTTGTGCTGTATTAAATATGAAAATGTTATTAA
ACATGTCTTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPHQASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMETYTL DLLECVTQRGHRRALARRVSSLRPLSVEILPPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAAVNLEPREHALLTLLLVYGPREGGRGAPDPFLGVKA AAAAE LERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~G~~CCAACGTGAGAGGAACCCGTGCGCGCTGC~~G~~C~~T~~T~~C~~TGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AACCATTTCTGTGCTT~~G~~ATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGAAAATTC
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAGAGACTTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTGATGGGTATACGCCCTAGGGCATTTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAAACTATTAATAAAATATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACTTTAGCTGTGTTCCCTTACTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCCTCTAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIIIVPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMVMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCAAATGTTCTTGTGACATTGCT
GGGATCCCCATCCTATTTCTCAGTCAGTCAGCTACCTGAGAATTCACAGAGCTCCTGCT
CTTCAAAACCTGTGATGAGAAAAAGTTCAGCTACCTGAGAATTCACAGAGCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGTCCATTGAAC TGGAATATTTCAATCC
AGCTGCTACTTCTTTCTACTGACACCATTCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTCGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAATCTCTTAAGAACAGAACAGGACAACCAAATGTGAAAGAAGGAAGAGCA
AGAACATGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATAAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGTGGCCCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCCTCGGCTGCCTGACTTCTTCCTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGAACGTCTTGATCATTACGGATTGCG
AGACAAGTGAACCCAGGATCGAGTGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAAGGGAGACTTGGCGGGTCTGTCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTCAGTGAAGCCAGTGAACCCCTGCTGTAGACTGCCAAGGCTGTACCACTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAAGGCCACCCCCGGCTCACTACAGCTGCTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCAGATTCTGCAATTCTCTTCACTTAAACTCTGAAACAGGCACITGGTGTCACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCATTCTCAATGACCGCAGGCTCAGCCAGGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGTTCTGGTGTCTGCTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGTACTTCATCAACAAATAACAGATGGAGAAAGTTACAAGA
ACCCAGGAAACAGATGGAGTTAACATCCGCACTGACGAGGAGGGCACTTCAGACACAAGTCATCGTTG
TGATCTGAGACCCCGGGTGGCTGAGAGCGCACAGAGCGCACGTGACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAGCTTTCTGTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAAGCCACATGAATAGAAGAAATTCTCAAGATGGACCCGGTAATATAACCACAA
GGAAGCAGAAACTGGGTGCGTTCACTGAGTTGGGCTTAATCTGTTCTGGCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTACGTAAACGCCGTGCTGGCCCTGTAAGGCCAGCATGTTACCAACTGGTGT
CAGCAGCCACGACACCAGTGAAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTGTTGCACTGTTGAGAAGCTTTGGATCAGCATTTGTAAGGAAACACAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGATCTGCTGAGGAACCTGCTTGTCCAACAGGGTGTAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTATTAAAGGAA
TACATCTAAATTGGTCTAAGGATGTTGATTGAAAGAAATTCTATTTAAACTGTAATATATTGT
CATACATGTTAAATAACCTTTTAAAGGTTCAACTTAAGGAGTTCAAGCTACTAGTGTAAAT
TGGAAATATCAATAATTAGACTATTTCACCAAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT
CACACAAAGTTAGCCTTTTCAAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCTCTTCAAAAGAACCTCTCAGGTTAGCTTGAAC
GCCTCTCCTGAGATGACTTAGGACAGTCTGACCCAGAGGGCACCCAGAAGGCCCTCAGATGACATACAGATG
CCAGTCAGCTCCTGGGGTTGGCCAGTGGCTGTCCAGTGTACGCTCCAGCTTGGCTCTGCTGCCCAGGAGGCC
GCCATCCTGGGGCTGGCAGTGGCTGTCCAGTGTACGCTCCAGCTTGGCTCTGCTTACAGCAGCACAGC
TCTCAGGTGGCACTGCAGGACACTGGTGTCTCCATGTAGCTTGGCTCTGCTGTAACAGACACTCT
TTTGTTATGGATGGCTACAAAATAGGGCCCCAATGCTATTTTTTTAAGTTGTTAATTATTGTT
AAGATTGCTAACGGCAAAGGCAATTGCAAAATCAAGTGTCAAGTACAATAACATTAAAGAAATGGAT
CCCACGTGCTCTTTGCCACAGAGAAAGCACCAGACGCCACAGGCTCTGCGATTCAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG
TGAAACGCCGAATCAAAAGCAGTTCTAATTGACTTTAAATTTCATCCGCCGGAGACACTGCTCCATT
TGTGGGGGACATTAGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGG
GAATGGCTCTCACTACTCACCTGTCTTCAAGCTTCAAGTGTCTGGTTTTTATACATTGACAGCTTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGAAACACTTGCCTGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCAAGCTCCAGCCTCCT
TCTTGGTTGTCTAGTGTAGGGTAGCCCTATTGCCCCCTCTTCTTACCCCTAAACCTTACACTAGTGCCA
TGGGAACCAAGGCTGAAAAGTAGAGAGAAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTGCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGGCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTTGTTAAC
CTCATTTATAAAAGCTTCAAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267